1

SEQ.I.D.NO:31

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   1 GTAAGAAAGG CATTTGCAAG AGATTGTGGC TGCTTATTTT GCCGCCCCCT

  51 TCCGACGGGC CCGCCGGGGG TAGCTGAGAG GCCCACCAGG GTTGCGGGAG

 101 AAACCGAACC GGGTGGGGGG AGGGTCCGAC TTGGAGGGGC GAGGGGGAAG

 151 ACCCACGGCC GACGCGGCCA CCAGGTCGAG GCGGAGGGTA GGGACAGCCC

 201 GGCTAGGGTC AGGCGTGCGA GGTCTGTTAC GAGGCCTCGA CCCGAGGCGG

 251 TGCCATGCGC GAAGCCCCGG CGCTGAGTGG CGAGACGGGG TCGCGACCTG

 301 GCGTGGGAAA GAAAGGTGGA GGCGGCCGCC ACTATGTGTG GCCCAGAGCC

 351 GGCAGGTCCG GTTGCCTCCC TGTGCCGGGG GAGGGACGGC GCGCGGGGTT

 401 CCGGAGCATT CTGACGGTAC CACTCGCGAG AGGCGGGGGT GCCTGGTCCT

 451 TAGATCCAGT CACTTCGTCG CGGCTAAAAC ACGGGTCGGG GAGAAGAAAC

 501 CGGCCGTTCA GTGTGCTGGT TTTCTTGACG GCCAGGACTG AGCCTAACCC

 551 CGAGGAGCGG CCGCGTGAGG CACCAGGAGC CCACCCGGCG CCGGGCGGGC

 601 GGGTCCATTT TGCCGCACAA GCCGGGCTAT TGGCAAACTG CGGATGGGCA

 651 GGTCCACCTT CCTTCGGGGG TGAGCGGCCT GAGGTATGGG AGGGCGACGC

 701 TACTTCGCGA CGGGGGCGGG CGGGATGTGG ATTGTTCCAT GGAGGGGTGG

 751 GAGACRCCGC CGGGTGGTCG ARGGAGCGAG CACATGGTGG CCTGAGGCGT

 801 TCCCTCCCC CAGTCTGCTT CGCTTCTAAG TGTTGTGCAA TCTCCCCCTT

 851 TGCTAGCTCG GCTTGGGCTC ATTGTGCGCG AGGCCGCCAC CGCCCGCGGC

 901 CTCCCACATC CGGGCAACGC GAGGGGGGGG CTTCGGCTGG AGGGAGTGGG

 951 GGAGGGCGCG GGCGGGATGA CGTGGGGGGA AGGGGATGTC CTACCCTCCG

1001 ATCTGGGAGG TGAAGGGCGG GACTTCCAGC GCGCTGGTGC TGCGGTGGGA

1051 GGTGCACGCG CTTGGGCTTT AAGCGGCTGG GTCGGGCCCA CGTGGACCCG

1101 GCGGCAAGCA CCACCTNTGG GCACCGTGAG CGCGGCGGCA CGCCTGCCGG

1151 CCTGTCTTCA GAAAGGGTCA CCCCCTTATG TCGGGGGTGG CCTGGCCTGA
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2

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1201 GCCGCTGCCT GCATGGGGCA AATGCCTCAG TTTTATAGAA ACTCCTCCTT

1251 TGGGTATTTT TTGGGAGCTG GTGGGAGTTG GATCTGGGAC AGCAGGTTGA

1301 TGGCATCATG CAGGCCACTC CTGACAGAGC CCGGCTGTCA GGATTTCTGA

1351 GTGCTTCGGT CGGGCAGGGG ACAAAACTTA TGCTTTAAAC CAACAG
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3

SEQ.I.D.NO:32

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  1 GTGAGACTGG AGAAATGGAA TTCTGTCCTC CCCCATTACA ACTTTCAGCC

 51 GTATAGAGTT AGAGTGGCCT CTTGATTGAT TTCCCAGATC ATCTAGAAGC

101 AGCTGGTTTC CCTAAAGGGA GGAGGGTTGT AAGCTCTGAG GCTTTTGTTA

151 RTASGCACCA SATTCTGTTT GCTCGGAGAC TACAGCTCAG CTCCACCTTT

201 TCCATGACTC AAGCTTTAAT TTCTTTGCAT CCCCTAG
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4

SEQ.I.D.NO:33

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  1 GTGAGACCTC TCAGTCCCAG ATGCCCATCT CATATCAGCC AGGGACAAAG

 51 CAACTCCTTG TTCATCCCAG CTTGGCTTTT GATCCGTGCC CATGCCTGGT

101 TCATGCCTTG GACACATAGG TTTCCTTTAA AGAGGTGGTA TTGTAGCCAG

151 CTTATATTTG CATCTACAGC CATGTTTCTA GTCCAGCTTG GTGTGCAATA

201 CTAGATGAGT TAATAACTGG TCCTTGTTTC TGATCTGGTT CCCATTGTGT

251 AACTGTGTTG ATTGGGAAGG TAGTTTGTGA GCCATGAAAT GCTTGGTTCA

301 TTGGTTGCTT ATTGACCTCA TTAACCTAGG ACTTGAATAT CCCAAAGGGT

351 ATGCTCTTTA CCACATTCAA CTCCTAATTT ATTTGTTTAG
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5

SEQ.I.D.NO:34

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  1 GTGAGTAATT CGGTTCTCCA ATCCCCTGGG TCACTTTGCT CTTGTGCACG

 51 CTTTCCAGTC TTTCAGCGTA AGCCAGAGTC ATTCCCAAGG ATGCTGGTTT

101 CTCTCTGGGG GAAGAGCTGC TCTGTGATGG AGCCCATGCG TGTCATCTGA

151 GCCTCTGGCT TCCCTGCCAG TGCAGCCCTG GCAGTGTCCT ACTTCCCAGG

201 GCTGTTGTCT GCCTGGCGGG AAGGTCCTGG GCAAAGGATC AGTCTTTGTA

251 CTCTGAGAGC AGACTACTTG GCTCCTCTCT GTTTTTTATC AGCGAAGTTG

301 GATATATCTC TCCCACATTT CCCTAATCAT ATGCTATATA TTGGCTTTTT

351 TTTTCTTCTC TAG
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6

SEQ.I.D.NO:35


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  1 GTGAGGGCAG  TCTTGCTTGA  ATAGCTAATG  ATTCTTGAAA  AATAGTAAGT

 51 GCCAGGGGAA  ACCAAATACT  GGATTCTTGA  GCCTTTTTAT  GCATCTGCTT

101 CAGTTTTAGG  TGTGGCTAGG  GAAGGGAGCA  GGCCTCAGGA  AGGAACCAGC

151 ACTCTAAGAC  TGGCCTTTTT  TTCCACTAG
```

7

SEQ.I.D.NO:36

1 GTGGGGCCCA GTGCAGGAGG CGGGCCTGGT AGTGAGTTGT TGGGTATAGC

51 CCCTGACTGA TTTTTGTCCC CCAACCTCCA G

8

SEQ.I.D.NO:37

```
  1 GTGAGTAGAG GGAACTGATA GCAAAGGCAG AAGGGAGGAT CCAAGGTGAT

 51 TCCCTCTCCA AGGGGACATC AGTGCCTCTC AGGAAAGTAG CAGCTTGGAA

101 TAGAATCTGG CATGCCTAAG GCCTTGGGG AACTGGGATG CTTATTTCCT

151 CTGCCTTCCT TGGCTGCCCA CATGGATGCC TAAGTGTCTT CCCTCCGGGA

201 TAGAGTGTCC TCCGTGCACA TGCTGAAGAG TTGTCTTTCT TGACGTAG
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9

SEQ.I.D.NO:38

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  1  CTACGATATC  GCTGTTGATT  TCCTTCATCC  CCTGGCACAC  GTCCAGGCAG

 51  TGTCGAATCC  ATCTCTGCTA  CAGGGGAAAA  ACAAATAACA  TTTGAGTCCA

101  GTGGAGACCG  GGAGCAGAAG  TAAAGGGAAG  TGATAACCCC  CAGAGCCCGG

151  AAGCCTCTGG  AGGCTGAGAC  CTCGCCCCCC  TTGCGTGATA  GGGCCTACGG

201  AGCCACATGA  CCAAGGCACT  GTCGCCTCCG  CACGTGTGAG  AGTGCAGGGC

251  CCCAAGATGG  CTGCCAGGCC  TCGAGGCCTG  ACTCTTCTAT  GTCACTTCCG

301  TACCGGCGAG  AAAGGCGGGC  CCTCCAGCCA  ATGAGGCTGC  GGGGCGGGCC

351  TTCACCTTGA  TAGGCACTCG  AGTTATCCAA  TGGTGCCTGC  GGGCCGATGT

401  CTGCGAGCCA  GGATTCCCG
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10

SEQ.I.D.NO:39

-526 CTACGATATC GCTGTTGATT TCCTTCATCC CCTGGCACAC GTCCAGGCAG

-476 TGTCGAATCC ATCTCTGCTA CAGGGGAAAA ACAAATAACA TTTGAGTCCA

-426 GTGGAGACCG GGAGCAGAAG TAAAGGGAAG TGATAACCCC CAGAGCCCGG

-376 AAGCCTCTGG AGGCTGAGAC CTCGCCCCCC TTGCGTGATA GGGCCTACGG
     c-ets1   Sp1

-326 AGCCACATGA CCAAGGCACT GTCGCCTCCG CACGTGTGAG AGTGCAGGGC

-276 CCCAAGATGG CTGCCAGGCC TCGAGGCCTG ACTCTTCTAT GTCACTTCCG
                                                  c-ets/Elk-1

-226 TACCGGCGAG AAAGGCGGGC CCTCCAGCCA ATGAGGCTGC GGGGCGGGCC
                                              Sp1

-176 TTCACCTTGA TAGGCACTCG AGTTATCCAA TGGTGCCTGC GGGCCGGAGC
                                      AP-2

-126 GACTAGGAAC TAACGTCATG CCGAGTTGCT GAGCGCCGGC AGGCGGGGCC
                 CRE-BP   AP-2   Sp1

 -76 GGGGCGGCCA AACCAATGCG ATGGCCGGGG CGGAGTCGGG CGCTCTATAA
      Sp1   Sp1

 -26 GTTGTCGATG GGCGGGCACT CCGCCCTAGT TTCTAAGGAT CATGTCTGCG
                                                  metserala

+24 AGCCAGGATT CCCG

    serglnasp ser

11

SEQ.I.D.NO:40

-5280 GCGGCCGCAT AATACGACTC ACTATAGGGA TCTAGGAAGG CCTCTCATAG

-5230 CTGAGACGTG AATGATGAGC AGCCAGCCAT GCGCAGACCT GGGAATAGCA

-5180 AGTACACAAG ACCCATAGTG AAAAACCATG GCTGAGGAAC AGAGGGCTTG

-5130 TGGGGGTGAC CTGTGTAGTT GGCGCAGAGT GAGCAAAGGG AGATGGATAC

-5080 AAAATTCGGT CAGAGAGTAG ATCATGTAAG ACATGTACGG TAGGCTGAGG

-5030 AGGGGGGATT TTATTGCGTG TATACTGAGA AGCCATTGAG TTTTAAGCAG

-4980 GCTGAGAAGT GCCTTCTGTT TTAAACTCCT GTTTCAATGA CAGATTGAAA

-4930 GGGGGGCAAG AATGGAAGCA GGAACAGAGC ACAGTAGTCC AGGTGAGAAA

-4880 CTTGAACTGG AGTGCTAAAG GAAGAGAGAG AGAGTAGTTT TATGTAGGAT

-4830 AAATTTTACG AGTAAAACCA GTAGGACTGA CAGGCTCTGT GATACTGAGA

-4780 GATACATATT TGTCTCCTGA CCAGGCTCCT GGCATTCAAC TTCTAAAATC

-4730 CTTGGAATCT CCAGTGATGT GTGTTTTGT GTGCTGATGA GTTGATTCAT

-4680 GGCTAGCCCC TCTAGGTGGC TTCATGATTA GAGGGTTGGA ACTTTCAGCC

-4630 TCACCCCCAC CAACTTCCTG GGAGGGGAAT GGGGCCA<u>AAG GTTAAGGCAA</u>

-4580 <u>TCACTGAGGA TCAGTGATTT AATCAGTCAT GCCTAGTAGT GAAGCCTCTA</u>

-4530 <u>AAAACCGGAA AGGGGCCGGG TTGCGCGGCG CACGCCTGTA CTCCCGGCAC</u>

-4480 <u>TTTGGGAGGC TGAGGCAGAT GGATCGCAAG GTCAAGAGAT TGAGACCAGC</u>

                          Alu I repeat

-4430 <u>CTGGCCGACC TGGCGAAACC CTGTCTCTAC TAAAAATATG AAAATTAGCT</u>

-4380 <u>GGGCGTGGTG CGTGCGCCTG TAGTCCCCGG GAGGCTGAGG CAGGAGAATC</u>

-4330 <u>GCTTGAACCC GGGAGGCAGA GGTTGCAGTG AGCCGAGATT GTGCCACTGC</u>

-4280 <u>ACTCCACCCT GGGTGACAGA GTGAAACTCT GTCTCAAAAA AGAAAAAAAA</u>

-4230 <u>A</u>CCCGAGAGG AGGAGTTTGG AGACATTCTA GATAGCTGAA GGCATGGAGG

-4180 CTGCCCACAG GATGGTCTGC CAGGCCTCTT CCCGGTACCT TTCCCTGTGC

12

-4130 ATCTTTTCAT CTGTACTCTT TGTACTACCC TTTGTTAATA AACTGGTAAA

-4080 TGTGTTTCCA TGAGTTCTGT GAGCTGCTCT AACAAATTAA TCAAATTCAA

-4030 GGAGGGGGTC ATGGGAACGC TGATCTAACC AGTTGGTGAG AAACACAGAT

-3980 AAAACAACCT GGGGCTTACG ACTGGCATCA GAATTGGGGG CAGCCTTGTG

-3930 AGACTGAGCC CTAAACCTGT GACACATTAT CTCCAGGTAG ATAGTGTTGG

-3880 AATTGAATTG GGGGATACCC AGCTGTGTCC ACCGCAAAAT TGCTTGCTTG

-3830 GTTGTTGGTG GAGAGAAAGC CCCACAAACA CTTCTTGGTG ACCACAGGTT

-3780 ACAGAAGTAT TTTGTGTTGT GAGAGTATAG TAGGAAAGAA GATTTGTTTT

-3730 TTTGCCGGGC GCGGTGGCTC ACGCCTGTAA TCCCAGCCCT TTGGGAGGCT

-3680 GAGGCGGGCG GATCACCAGG TCAGGAGATC AAGACCATCC TGGCTAACAC

-3630 AGTGAAACCC TGTCTCTACT AAAAATACAA AAAATTAGCC GGGCGAGGTG

                        Alu I repeat

-3580 GCACGTGTCT GTAGTCCAAG CTACTTGGGA GGCTGAGGCA GGAGAATGGC

-3530 ATGAACCCAG GAGGTGGAGC TTGCAGTGAG GCAAGATCAC GCCACTGCAC

-3480 TCCAGTCTGG GCAACAGAGC AAGACTCCGT CTCAAAAAAA AAAAAAAAA

-3430 AAAAGATTTG TTTTTTCCTC TGCAGGTTGG ATGTGGGAAA TGAAGAAAAA

-3380 GAAATGGAGG ATGATGCCTA GGTTTTTGGC CTATGTAACG GGAAAAGTGG

-3330 GAGAGGAACA GGTTGGGGGA GGAAAATGAA GAGTTCTTTT CTCTTCTGGT

-3280 TTCCCTGCCC TCCCATTCAA AAGCCAGGAA ATTTCTACAG CTAGGCAGGA

-3230 TGATTGGCTC CGGCATTCCT TAATTTCAGT CCTCAAAATC AAGAGCTTAC

-3180 ACCCTCAGGG ATCTTCTTGC AGTAGAGGGA AGGGTGGTGA CGTACAGTGA

-3130 AAAACATGTT GGCCTTCTTC ATACTGAGTT TGAGTCCCAC TTCTGCCATT

-3080 TCTTTCTTTC ATGACCTTGT GCAAGTCACG ACTTTCCAAG CTGCAATTTC

-3030 CTCATCTGTT AGGTTGAATG TTGAGAACTT CCCGGTAGGA TTGTTATGAG

-2980 CATTAACTGC GTGTTTACTT TGTGCTGTGT CTTGTTCTAA GTGTATTATG

-2930 GATAGTCACT AGTTTAATCC TCATATCAAA TGGATGAGGT GTAGGTACTA

-2880 CTATTTACAC TCTCTGACAG ATAAGGAAAC TGAGGTATAG AAGGTTATTA

13

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-2830 AGTAGGTTGC CCACTGTCAT AAGCCAGTAA ATGGAGGAGC TGTATTTGAA

-2780 TTCTGGCAGG CTCCAGAATC CTGGGCCTGG GTTCTTAGCT GCTAAGTGCT

-2730 TCTCCCTTTA AAGTGTGAAA AGCGCCTGCC CATCATGGGT TCTCAAGTGT

-2680 TCGTTCTGAT GTCTCCTCCA TTGTCTGACC TTCCTCCCTT ACCCCGAAGA

-2630 ACCGAAACAT GCAGATCCTG AGCTTGCCCA CAATCTAGGC CTTGGGTCTT

-2580 CTGTTCTTTC ACTTGGTTCC CTTACCTGTG TCTCTGTTCC TCTCTAGAAC

-2530 CTTCATGGCA AAAGGCAAGA CTTCTGTTTG TTGTACCTGA CCTGTGGCAC

-2480 TATCTCTTTA GGTGGACATC TTCAATAAGG AGCTACTGCT AATCCCCATC

-2430 CACCTGGAGG TGCATTGGTC CCTCATCTCT GTTGATGTGA GGCGACGCAC

-2380 CATCACCTAT TTTGACTCGC AGCGTACCCT AAACCGCCGC TGCCCTAAGG

-2330 TTTGAGGGGG TAGGAGAGAG ATGGGCAAAA TGTGGGGCGG TGCAGTGGCA

-2280 AGGCATTGCA GGAAGAAGGG TGGGCTTTGG GTCTTTGAGG GGCGACCTGG

-2230 GCATGGTGTC TGCCAGCACT GTACCCACCA TACTGTGTTC AATTGAGAAA

-2180 CTTAGGGCAT CACTTTCTTT TCCCCCATCC ACATAGCATA TTGCCAAGTA

-2130 TCTACAGGCA GAGGCGGTAA AGAAAGACCG ACTGGATTTC CACCAGGGCT

-2080 GGAAAGGTTA CTTCAAAATG GTGAGTTTCC TGAGGGAGGG GTATAGGGTG

-2030 TTGGTGGGGA CAGTGGTAGA AGGCAGAAAT TGAAGTCCTA CCCCTGGGAG

-1980 TCTCCATGTG AAGGGCCTGC TTTCTTTCTC TTCTCTAGAA TGTGGCCAGG

-1930 CAGAATAATG ACAGTGACTG TGGTGCTTTT GTGTTGCAGG TAAGCAGATG

-1880 ATGGGGCCAC CTCCTCTAGC TCTGAAGTCA GTTGGGTTAA AGGGTCGGGA

-1830 GGCTGTTATG CATCCCCTCA TTTGGCTCAT AGTCAGTTGT GGAGCAGGAA

-1780 GTAATCTGTT TTAGAACACC AAAACACTGG CTTCACTGGT TCTCTTCTGG

-1730 ACTTCTCCAT CCCACATTGG GACTGGGTCT CTAGGTCTTT TGGCTCTGGC

-1680 CTTCATAGAG CTCCCTGCTA ACCTCCAACT CAGTGTATTT TCTCCATCTA

-1630 AAACATTCTA TCAAGTAAGA ACACTAGCTT TAGAGTCAGG CTGTTTTTGA

-1580 ACCCCAGGCT GTGGGACCCT GGCTCCCTTT GGGGATGTTC TCTGAAGGAT

-1530 GGAGACACAT CTCATATGAA ATGTGTAGCA CAGGTCCTGA CACGGGGGGT
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14

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-1480 TTCTCATGGC TTGCTTTGTT AACACCCAGT ACTGCAAGCA TCTGGCCCTG

-1430 TCTCAGCCAT TCAGCTTCAC CCAGCAGGAC ATGCCCAAAC TTCGTCGGCA

-1380 GATCTACAAG GAGCTGTGTC ACTGCAAACT CACTGTGTGA GCCTCGTACC

-1330 CCAGACCCCA AGCCCATAAA TGGGAAGGGA GACATGGGAG TCCCTTCCCA
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Homology to mouse eIF4A gene sequence

```
-1280 AGAAACTCCA GTTCCTTTCC TCTCTTGCCT CTTCCCACTC ACTTCCCTTT

-1230 GGTTTTTCAT ATTTAAATGT TTCAATTTCG TGTATTTTTT TTTCTTTGAG

-1180 AGAATACTTG TNTATTTCTG ATGTGCAGGG GATGGCTACA GAAAAGCCCC

-1130 TTTCTTCCTC TGTTTGCAGG GGAGTGTGGC CCTGTGGCCC TGGGTGGAGC

-1080 AGTCATCCTC CCCCTTCCCC GTGCAGGGAG CAGGAAWTCA GNGATGGGGG

-1030 GNGGGGGGCG GACAATAGGA TNACAGCCCG CCAGATATNC ATATATATAT

 -980 ATATATATAT ATATATATAT ATATATATAT ATATATATAT ATATATATAT

 -930 ATATATATAT ATATATAAAA ATGCCACGGT CCTGCTCTGG TCAATAAAGG

 -880 ATCCTTTGTT GATACGTAAG TGGTGGTCTT CCTTAAGGGG CTTCAAATTA

 -830 GTGGATATGC TTAGCTCAGA CCTTCCAGCC AGTNTCTTGA GACTAAAGGG

 -780 TTCAGCTTTC CATCCCTGGC TCAGGCACTG CCAACACCTT GTCTTCACCC

 -730 AAACAAATCC CCCAGATGGG AGCAGAGAGC AGGAAGGAGG GAAAGTAGAT

 -680 AAGCCTCAAG AATAAGGGCA TCCGAGAGGG AAGCGTGGGG AACTGGACAC

 -630 AAGGGACTGG GGAGGGGACC AACCAGGATT CATGATAGTA CCCCAAAGCC

 -580 CTTTACAGTT TTYTTCCATC CCTCCACCAT CCAGCCAGGG GAATCCTCCC

 -530 ATCCCTACGA TATCGCTGTT GATTTCCTTC ATCCCCTGGC ACACGTCCAG

 -480 GCAGTGTCGA ATCCATCTCT GCTACAGGGG AAAAACAAAT AACATTTGAG

 -430 TCCAGTGGAG ACCGGGAGCA GAAGTAAAGG GAAGTGATAA CCCCCAGAGC

 -380 CCGGAAGCCT CTGGAGGCTG AGACCTCGCC CCCCTTGCGT GATAGGGCCT

 -330 ACGGAGCCAC ATGACCAAGG CACTGTCGCC TCCGCACGTG TGAGAGTGCA

 -280 GGGCCCCAAG ATGGCTGCCA GGCCTCGAGG CCTGACTCTT CTATGTCACT

 -230 TCCGTACCGG CGAGAAAGGC GGGCCCTCCA GCCAATGAGG CTGCGGGGCG
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Homology to mouse eIF4A gene sequence

-180   GGCCTTCACC TTGATAGGCA CTCGAGTTAT CCAATGGTGC CTGCGGGCCG

-130   GAGCGACTAG GAACTAACGT CATGCCGAGT TGCTGAGCGC CGGCAGGCGG

-80   GGCCGGGGCG GCCAAACCAA TGCGATGGCC GGGGCGGAGT CGGGCGCTCT

-30   ATAAGTTGTC GATGGGCGGG CACTCCGCCC TAGTTTCTAA GGATCATGTC

+20   TGCGAGCCAG GATTCCCG